SEQUENCE LISTING

<110> DAUGHERTY, BRUCE L.
DEMARTINO, JULIE A.
SICILIANO, SALVATORE J.
SPRINGER, MARTIN J.

<120> NUCLEIC ACID ENCODING EOSINOPHIL EOTAXIN
RECEPTOR

<130> 19634YDACA

<140> 10/767,521
<141> 2004-01-29

<150> 60/016,158
<151> 1996-04-26

<150> 09/922,895
<151> 2001-09-06

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 355
<212> PRT
<213> Human

<400> 1

```
Met Thr Thr Ser Leu Asp Thr Val Glu Thr Phe Gly Thr Thr Ser Tyr
 1               5                  10                  15
Tyr Asp Asp Val Gly Leu Leu Cys Glu Lys Ala Asp Thr Arg Ala Leu
                20                  25                  30
Met Ala Gln Phe Val Pro Pro Leu Tyr Ser Leu Val Phe Thr Val Gly
            35                  40                  45
Leu Leu Gly Asn Val Val Val Val Met Ile Leu Ile Lys Tyr Arg Arg
        50                  55                  60
Leu Arg Ile Met Thr Asn Ile Tyr Leu Leu Asn Leu Ala Ile Ser Asp
65                  70                  75                  80
Leu Leu Phe Leu Val Thr Leu Pro Phe Trp Ile His Tyr Val Arg Gly
                85                  90                  95
His Asn Trp Val Phe Gly His Gly Met Cys Lys Leu Leu Ser Gly Phe
                100                 105                 110
Tyr His Thr Gly Leu Tyr Ser Glu Ile Phe Phe Ile Ile Leu Leu Thr
        115                 120                 125
Ile Asp Arg Tyr Leu Ala Ile Val His Ala Val Phe Ala Leu Arg Ala
        130                 135                 140
Arg Thr Val Thr Phe Gly Val Ile Thr Ser Ile Val Thr Trp Gly Leu
145                 150                 155                 160
Ala Val Leu Ala Ala Leu Pro Glu Phe Ile Phe Tyr Glu Thr Glu Glu
                165                 170                 175
Leu Phe Glu Glu Thr Leu Cys Ser Ala Leu Tyr Pro Glu Asp Thr Val
```

```
                    180                 185                 190
Tyr Ser Trp Arg His Phe His Thr Leu Arg Met Thr Ile Phe Cys Leu
        195                 200                 205
Val Leu Pro Leu Leu Val Met Ala Ile Cys Tyr Thr Gly Ile Ile Lys
    210                 215                 220
Thr Leu Leu Arg Cys Pro Ser Lys Lys Lys Tyr Lys Ala Ile Arg Leu
225                 230                 235                 240
Ile Phe Val Ile Met Ala Val Phe Phe Ile Phe Trp Thr Pro Tyr Asn
                245                 250                 255
Val Ala Ile Leu Leu Ser Ser Tyr Gln Ser Ile Leu Phe Gly Asn Asp
            260                 265                 270
Cys Glu Arg Ser Lys His Leu Asp Leu Val Met Leu Val Thr Glu Val
        275                 280                 285
Ile Ala Tyr Ser His Cys Cys Met Asn Pro Val Ile Tyr Ala Phe Val
    290                 295                 300
Gly Glu Arg Phe Arg Lys Tyr Leu Arg His Phe Phe His Arg His Leu
305                 310                 315                 320
Leu Met His Leu Gly Arg Tyr Ile Pro Phe Leu Pro Ser Glu Lys Leu
            325                 330                 335
Glu Arg Thr Ser Ser Val Ser Pro Ser Thr Ala Glu Pro Glu Leu Ser
        340                 345                 350
Ile Val Phe
        355
```

<210> 2
<211> 1065
<212> DNA
<213> Human

<400> 2
```
atgacaacct cactagatac agttgagacc tttggtacca catcctacta tgatgacgtg 60
ggcctgctct gtgaaaaagc tgataccaga gcactgatgg cccagtttgt gcccccgctg 120
tactccctgg tgttcactgt gggcctcttg ggcaatgtgg tggtggtgat gatcctcata 180
aaatacagga ggctccgaat tatgaccaac atctacctgc tcaacctggc catttcggac 240
ctgctcttcc tcgtcaccct tccattctgg atccactatg tcagggggca taactgggtt 300
tttggccatg gcatgtgtaa gctcctctca gggttttatc acacaggctt gtacagcgag 360
atctttttca taatcctgct gacaatcgac aggtacctgg ccattgtcca tgctgtgttt 420
gcccttcgag cccggactgt cacttttggt gtcatcacca gcatcgtcac ctggggcctg 480
gcagtgctag cagctcttcc tgaatttatc ttctatgaga ctgaagagtt gtttgaagag 540
actctttgca gtgctcttta cccagaggat acagtatata gctggaggca tttccacact 600
ctgagaatga ccatcttctg tctcgttctc cctctgctcg ttatggccat ctgctacaca 660
ggaatcatca aaacgctgct gaggtgcccc agtaaaaaaa agtacaaggc catccggctc 720
attttttgtca tcatggcggt gtttttcatt ttctggacac cctacaatgt ggctatcctt 780
ctctcttcct atcaatccat cttatttgga aatgactgtg agcggagcaa gcatctggac 840
ctggtcatgc tggtgacaga ggtgatcgcc tactcccact gctgcatgaa cccggtgatc 900
tacgccttt ttggagagag gttccggaag tacctgcgcc acttcttcca caggcacttg 960
ctcatgcacc tgggcagata catcccattc cttcctagtg agaagctgga aagaaccagc 1020
tctgtctctc catccacagc agagccggaa ctctctattg tgttt 1065
```

<210> 3
<211> 3586
<212> DNA
<213> Human
```

<400> 3

```
ggatccctac cttcccçatc agagctaggg ggcatggagc gctctctgct aagatgggga 60
cccccaagga atgtctccct gtggggcact tccttaccag atgggatggc cagtgcggtt 120
aagttggtgg tcaggcagaa aaaaaagatc tagtttgtac tcttgagagt tcctcggttt 180
gttcatggca tgggcaggga gtcaaggagc agcagccttg cctcagtgcc taccagtgca 240
ggaaaaggtg catagcctgg gccagggcca gggccctggt ggaggcgtag tggtaacaga 300
gagggctctc cattccagcc caaggaagac taagaatgaa tacctcatga gtatattagc 360
tacaaaccac cacagcaggt tccagaaaaa ggctcagcgt tggaaccagg tcacccccac 420
tcagcagaca ccagtcatat aaatcaagga ccaacaggag acaggaacac ccccttccca 480
ctctgcccca tgtctcaagt tgtagtggcc cttcctccag atctctgcca ccatcttaga 540
aaggaacact gaaagaagaa actgaaatta taagctgaca gcataaagag gatgagtaaa 600
acctaaaatc attgttcaca tgaatgaatc aagagaagtt taaaccactt tggactaaaa 660
tgtgtgaatc cttttttcctg ctatccagca gatgagaagc tggtaacaga gaccacaata 720
gtttggagac taaagaatca ttgcacattt cactgctgag ttgtattgtg agtaatttta 780
gttgacctca ctttgtaaat cttgcacacg gggcaatcca atatctgcac aagagatatg 840
ttaaccagtg gtaaatgctg catgaggaga ttgggtgatt tttactttcg ttttttgtgct 900
cttctttctt attgttctta cttatttacg attaccctat cgttttccca aaatgtaaaa 960
ggccattttg aaagcctaat tcaaacctct tcactatttt gtatctaagt attcaccttg 1020
attgagactg ggtagacagg tgaaaaccat atcaggtttt taattttttta attttttaatt 1080
atttatttat ttatttattt tttgagatgg agtctggctg tcgcccaggc tggagtgcag 1140
cggcgtgatc acagttcact gcagcctcaa ccttctaggc tcaagggatt ctcccacctc 1200
agccccccaa gtagttggga ccacacgtat gcgccaccat gcctggctaa tttcttattt 1260
ttttgtagag ataggatctc actatattgt ccaggctggt cttgaattcc tgggctcagg 1320
tgagcctccc acctgggcct cccaaagtac tgggattaca ggcatgagcc aaggtcccct 1380
gcccatatga gattttctgt ctctgatccc atgcagctag taatcaagga cttggctgct 1440
gactctggag gacctgcatg ctttcttgag ctgtgaactt cagtgctaaa agctcatagg 1500
cagccctgaa acccaaacca aaaggttcta tggtttatca tcctgatcat gttgatttta 1560
tagaaataac acatgaatta aagacactac cctcaaactg agcaaaactt aagtaatttt 1620
tttaaagttt gacctgtttt taaatcactc ttggagaaaa aggaaaataa atacaaataa 1680
ttaacggtga atacaggcta ctataccttt gttctccaga attagcagtt ctgttctttt 1740
cttgctttag atgctgaagt gcagaaggac actctgtgat tgtacgtgtg taactgacaa 1800
aatgtgtatt ttttttctca gctgctatgg attggattat gctattatga ataagaatgc 1860
tgatgggagc acacacaaac catttgttcc tcagtccatt ttcctcctca aaagcctgga 1920
atgtgccatt gatcagtggg agatgtacct ggacagaccc atgaaaagag atcaacaagt 1980
tccacccaag ggaccctatt tttcctaatt tcatttgaaa tggcttctaa ttgtccttct 2040
ttcattcctg cttcctacca gttttacagc ttttttctggt ttcaaatgtg aactcacata 2100
cactctcatt tttcctcatc acaaccccaa gtgacccaat ggtcctcact ttcgatataa 2160
gtaaaggagg ctctgcatta agggcttgtc caaggcacgc agctgagagg cgctaggact 2220
ggctccattt ccatctctat tctcactgac tttgactacc cagaacccca acatgtgggg 2280
cctcagtatt cgatcaatta ttctattaag aagcaaaaac aattccccgc attggcccca 2340
gttattaagc atttctcaga tttaccttga gaaatgccca tcggcctgta tattcacatc 2400
ttcacccttg tcccttcctc ctagaaagga gaaagtcagt ggatgccct ctgaggaact 2460
agtgcatggc ttaactgtcc ttccatgact cctgccttat ctgtttttcta ttttcctcct 2520
tttccaccga agtctataat ctcaagaaaa gcaggcactg gccttagggc tcctggccta 2580
agaaatatca agtccagtga gaaatcccat tgactgaccc ctcctgctta cccctttgtg 2640
atggagaagc tcccaggggt ttgcttttttg catgttacca ggcctaactc agcatcacca 2700
ggggcaagaa aaggaaagta acctaaacta atgctgctta taattgtaat tattgtaata 2760
gttaattact gtgattgtac atgtgtaaca gacaaaatgt gtattttttt cacagctgct 2820
gtggattgga ttatgccatt tggaataaga atgctgttaa gagcacacaa gccaggttcc 2880
tcaagtccgt agcaaatttt tcaaaagtta aatttaaaaa tcactacatt tgaatctagt 2940
gacaggagaa atggacatgg atagagacta aagatctagc ccaaatttta tatttacttg 3000
ttagaggatt ttgaacaaat tactaaattt cttcaaggtt caatttcccc attaactata 3060
atgaatgtct catcattatg gggccctgga gaagcataat tacttgtaat tgtaataatc 3120
attgttatta ttattataca tattttgctt ttaaatggat aaggattttt aaggtatatg 3180
taaactgtaa aacataaaat gcaaaatgcc gtaagagaca gtagtaataa taatgattat 3240
```

```
tatattgtta tcattatcta gcctgttttt tcctgttgtg tatttcttcc tttaaatgct 3300
tacagaaatc tgtatccca ttcttcacca ccaccccaca acatttctgc ttctttttccc 3360
atgccggtca tgctaacttt gaaagcttca gctctttcct tcctcaatcc ttctcctggc 3420
acctctgata tgcctttga aattcatgtt aaagaatccc taggctgcta tcacatgtgg 3480
catctttgtt gagtacatga ataaatcaac tggtgtgttt tacgaaggat gattatgctt 3540
cattgtggga ttgtattttt cttcttctat cacagggaga agtgaa          3586

<210> 4
<211> 448
<212> DNA
<213> Human

<400> 4
taggtcagat gcagaaaatt gcctaaagag gaaggaccaa ggagatgaag caaacacatt 60
aagccttcca cactcacctc taaaacagtc cttcaaactt ccagtgcaac actgaagctc 120
ttgaagacac tgaaatatac acacagcagt agcagtagat gcatgtaccc taaggtcatt 180
accacaggcc aggggctggg cagcgtactc atcatcaacc ctaaaaagca gagctttgct 240
tctctctcta aaatgagtta cctacatttt aatgcacctg aatgttagat agttactata 300
tgccgctaca aaaaggtaaa acttttata ttttatacat taacttcagc cagctattga 360
tataaataaa acattttcac acaatacaat aagttaacta ttttatttttc taatgtgcct 420
agttctttcc ctgcttaatg aaaagctt                                  448
```